



Figure 1

Figure 2

Alignment of the *CAH* gene from *Myrothecium verrucaria* with a new cyanamide tolerance gene isolated from *Aspergillus* (CAH-H1) and a non-functional yeast *CAH* homolog (CAH-H2)

CAH	MSSSEVKANGWTAVPVSAKAIVDSLGLGVDVSSYSVEDIAFPAADKLVAEAQAFVKARLS	60
CAH-H1	MCQNEVEVNGWTSMPADAGAI FDGGPFINVPEALSIEEIKFPVDDPIVEKTMRYAKAALP	60
CAH-H2	-----MSQYGFVRVPREVEKAIP-----VVNAPRPRAVPPPNSETARLVREYAAKELT	49
	:. *:. :* .. . :. : * . . . :. *	
CAH	PETYNHSMRVFYW-----GTVIARRLLPEQAKDLSPSTWALTCLLHD	102
CAH-H1	TETFNHSMRVYYYGMQDCASHGVLINRSQALGMAITKQQFPKQASALSPSTWALTCLLHD	120
CAH-H2	APVLNHSRLRVFQY-----SVAIIRDQFP--AWDLQDEVLYVTCLLHD	89
	. . ***:***: : . .* : :* * * . . :*****	
CAH	VGTAEEYFTSTRMSFDIYGGIKAMEVLK-VLGSSTDQAEAVAEAIIRHEDVGVDGNITFL	161
CAH-H1	IGTSDHNLAATRMSFDIYGGIKALEVLK-GFGATSDQAEAVAEAIIRHQDLGVHGTITYI	179
CAH-H2	IATTDKNMRATKMSFEYYGGILSRELVFNATGGNQDYADAVTEAIIRHQDLTGTGYITT	149
	::*:: : :*:***: ***** : *:: *.. * *:***:*****:*: * ** :	
CAH	GQLIQLATLYDNVGAYDGDIDDFGSWVDDTTRNSINTAFPRHGWCWFACTVRKEESNKPW	221
CAH-H1	GQLIQLATIYDNVGAHPYVKDFGELIHDTTRSQVHEAHPPGEWRTFFSGVIQKEQAIKPW	239
CAH-H2	GLILQIATTLDNVGSN-----TDLIHIDTVSAINEQFPRLHWLSCFATVVDTENSRRKPW	203
	* :*:*** *****: . .. * . :. .* * : *: . : .*: : ***	
CAH	CHTTHIPQ-FDKQMEANTLMKPWE	244
CAH-H1	CHTKKMVN-VLRKGSRHPDGQ---	259
CAH-H2	GHTSSLGDDFSKKVICNTFGYN--	225
	** . : : . :. :. :	

Alignment between a new ubiquitin-like promoter (UbiN) and the corresponding part of the sugarcane Ubiquitin-4 promoter.

Figure 4. GUS-expression in *Agrobacterium*-infected alfalfa seedlings
“- vortex”: subjection by immersing (30 minutes) seedlings into an *Agrobacterium* suspension; “+ vortex” subjection by vortexing (30 minutes) seedlings immersed in an *Agrobacterium* suspension.

